

antigen-binding molecule which binds to VISTA and inhibits VISTA-mediated signalling, wherein the antigen-binding molecule comprises:

- (i) a heavy chain variable (VH) region incorporating the following CDRs:

HC-CDR1 having the amino acid sequence of SEQ ID NO:33

HC-CDR2 having the amino acid sequence of SEQ ID NO:34

HC-CDR3 having the amino acid sequence of SEQ ID NO:35;

or a variant thereof, in which one amino acid of HC-CDR1, two amino acids of HC-CDR2 and one amino acid of HC-CDR3 are substituted with another amino acid; and

- (ii) a light chain variable (VL) region incorporating the following CDRs:

LC-CDR1 having the amino acid sequence of SEQ ID NO:41

LC-CDR2 having the amino acid sequence of SEQ ID NO:42

LC-CDR3 having the amino acid sequence of SEQ ID NO:43;

or a variant thereof, in which one amino acid of LC-CDR2 is substituted with another amino acid.

59. The method according to claim **58**, wherein the antigen-binding molecule comprises:

- a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:32; and

- a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:40.

60. The method according to claim **58**, wherein the cancer is selected from: colorectal cancer, pancreatic cancer, breast cancer, liver cancer, prostate cancer, ovarian cancer, head and neck cancer, leukemia, lymphoma, melanoma, thymoma, lung cancer, non-small cell lung cancer (NSCLC) and a solid tumor.

61. The method according to claim **58**, wherein the method further comprises administering an agent capable of

inhibiting signalling mediated by an immune checkpoint protein selected from PD-1, CTLA-4, LAG-3, TIM-3, TIGIT and BTLA.

62. A method for inhibiting the activity of VISTA-expressing cells, comprising contacting VISTA-expressing cells with an antigen-binding molecule which binds to VISTA and inhibits VISTA-mediated signalling, wherein the antigen-binding molecule comprises:

- (i) a heavy chain variable (VH) region incorporating the following CDRs:

HC-CDR1 having the amino acid sequence of SEQ ID NO:33

HC-CDR2 having the amino acid sequence of SEQ ID NO:34

HC-CDR3 having the amino acid sequence of SEQ ID NO:35;

or a variant thereof, in which one amino acid of HC-CDR1, two amino acids of HC-CDR2 and one amino acid of HC-CDR3 are substituted with another amino acid; and

- (ii) a light chain variable (VL) region incorporating the following CDRs:

LC-CDR1 having the amino acid sequence of SEQ ID NO:41

LC-CDR2 having the amino acid sequence of SEQ ID NO:42

LC-CDR3 having the amino acid sequence of SEQ ID NO:43;

or a variant thereof, in which one amino acid of LC-CDR2 is substituted with another amino acid.

63. The method according to claim **62**, wherein the antigen-binding molecule comprises:

- a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:32; and

- a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:40.

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